

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/900,380
Source: FWO
Date Processed by STIC: 11/19/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

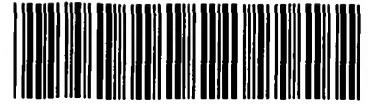
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/700,380</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 ____ Use of <220>	Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/700,380

DATE: 11/19/2003

TIME: 16:41:40

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11192003\J700380.raw

3 <110> APPLICANT: Timmermans, Eveline
 4 C.A.C.
 7 van Gemen, Bob
 W--> 8 <120> TITLE OF INVENTION: Method for Quantifying a Ratio Between at Least
 W--> 9 Two Nucleic Acid Sequences
 W--> 10 <130> FILE REFERENCE: 2183-5581.1US
 W--> 11 <140> CURRENT APPLICATION NUMBER: To be Assigned
 14 <141> CURRENT FILING DATE: 2003-11-03
 15 <150> PRIOR APPLICATION NUMBER: 60/425,055
 16 <151> PRIOR FILING DATE: 2002-11-08
 W--> 17 <160> NUMBER OF SEQ ID: 18
 18 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

W--> 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 48
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial sequence
 W--> 23 <220> FEATURE:
 24 <223> OTHER INFORMATION: Synthesized sequence, primer MtD
 25 pl
 W--> 26 <400> SEQUENCE: 1
 E--> 27 aattctaata cgactcacta tagggagaag
 28 agccgttgag ttgtggta 48
 29 <210> SEQ ID NO: 2
 30 <211> LENGTH: 25
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Artificial sequence
 W--> 33 <220> FEATURE:
 34 <223> OTHER INFORMATION: Synthesized sequence, primer MtD
 35 p2
 W--> 36 <400> SEQUENCE: 2
 E--> 37 tctccatcta ttgatgaggg totta
 38 25
 39 <210> SEQ ID NO: 3
 40 <211> LENGTH: 49
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Artificial sequence
 W--> 43 <220> FEATURE:
 44 <223> OTHER INFORMATION: Synthesized sequence, MtD pl_2
 W--> 45 <400> SEQUENCE: 3

pp 1-5
IMPORTANT: Please
 ensure that file is saved
 in ASCII text
 (per 1.824
 of Sequence Rules)
 (global error)
 see item 1 on Error Summary
 Sheet

same errors

RAW SEQUENCE LISTING

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Input Set : A:\PTO.YF.txt

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E--> 46 aattctaata cgactcacta tagggaagaa *same*
47 ccgggctctg ccattcttaa 49
48 <210> SEQ ID NO: 4
49 <211> LENGTH: 20
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial sequence

W--> 52 <220> FEATURE:
53 <223> OTHER INFORMATION: Synthesized sequence, primer MtD
54 p2_2 *same*
56 <400> SEQUENCE: 4

E--> 57 gtaatccagg tcggtttcta
58 20
59 <210> SEQ ID NO: 5
60 <211> LENGTH: 32
61 <212> TYPE: DNA
62 <213> ORGANISM: Artificial sequence

W--> 63 <220> FEATURE:
64 <223> OTHER INFORMATION: Synthesized sequence, primer MtD
65 mb_2

W--> 66 <400> SEQUENCE: 5

E--> 67 ggacccccca caccaccca agaacagggt cc *same*
68 32
69 <210> SEQ ID NO: 6
70 <211> LENGTH: 49
71 <212> TYPE: DNA
72 <213> ORGANISM: Artificial sequence

W--> 73 <220> FEATURE:
74 <223> OTHER INFORMATION: Synthesized sequence, primer SnrpD
75 p1

W--> 76 <400> SEQUENCE: 6

E--> 77 aattctaata cgactcacta tagggagagg
78 cccggcatgt ggtgcataa 49
79 <210> SEQ ID NO: 7
80 <211> LENGTH: 23
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial sequence

W--> 83 <220> FEATURE:
84 <223> OTHER INFORMATION: Synthesized sequence, primer SnrpD
85 p2

W--> 86 <400> SEQUENCE: 7

E--> 87 ttctttacat ctctacccg cta
88 23
89 <210> SEQ ID NO: 8
90 <211> LENGTH: 20
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial sequence

W--> 93 <220> FEATURE:
94 <223> OTHER INFORMATION: Synthesized sequence, primer
95 (SnrpD2 p2

RAW SEQUENCE LISTING

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11192003\J700380.raw

W--> 96 <400> SEQUENCE: 8

E--> 97 tgcgcctctt tctgggtgtt

98 20

99 <210> SEQ ID NO: 9

100 <211> LENGTH: 34

101 <212> TYPE: DNA

102 <213> ORGANISM: Artificial sequence

W--> 103 <220> FEATURE:

104 <223> OTHER INFORMATION: Synthesized sequence, primer

105 SnrnpD mb_2

W--> 106 <400> SEQUENCE: 9

E--> 107 cgcattgtgt aaccacgcac tctcctcgca tgcg

108 34

109 <210> SEQ ID NO: 10

110 <211> LENGTH: 34

111 <212> TYPE: DNA

112 <213> ORGANISM: Artificial sequence

W--> 113 <220> FEATURE:

114 <223> OTHER INFORMATION: Synthesized sequence, primer Mtr

115 mb

W--> 116 <400> SEQUENCE: 10

E--> 117 gctccgaagc ttctgactct tacctccccg gagg

118 34

119 <210> SEQ ID NO: 11

120 <211> LENGTH: 49

121 <212> TYPE: DNA

122 <213> ORGANISM: Artificial sequence

W--> 123 <220> FEATURE:

124 <223> OTHER INFORMATION: Synthesized sequence, primer Mtr

125 p1_4

W--> 126 <400> SEQUENCE: 11

E--> 127 aattctaata cgactcacta tagggagagg

128 agacacctgc taggtgtaa 49

129 <210> SEQ ID NO: 12

130 <211> LENGTH: 22

131 <212> TYPE: DNA

132 <213> ORGANISM: Artificial sequence

W--> 133 <220> FEATURE:

134 <223> OTHER INFORMATION: Synthesized sequence, primer Mtr

135 p2_2

W--> 136 <400> SEQUENCE: 12

E--> 137 ggtgcccccg atatggcggt cc

138 22

139 <210> SEQ ID NO: 13

140 <211> LENGTH: 49

141 <212> TYPE: DNA

142 <213> ORGANISM: Artificial sequence

W--> 143 <220> FEATURE:

144 <223> OTHER INFORMATION: Synthesized sequence, primer Sig

RAW SEQUENCE LISTING

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Input Set : A:\PTO.YF.txt

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145 pl
W--> 146 <400> SEQUENCE: 13
E--> 147 aattctaata cgactcacta tagggagagg
148 actggggccct cagcctgca 49 *same*
149 <210> SEQ ID NO: 14
150 <211> LENGTH: 21
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial sequence
W--> 153 <220> FEATURE:
154 <223> OTHER INFORMATION: Synthesized sequence, primer Sig
155 p2
W--> 156 <400> SEQUENCE: 14
E--> 157 ctgaggagac aagcaccatc a *same*
158 21
159 <210> SEQ ID NO: 15
160 <211> LENGTH: 32
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial sequence
W--> 163 <220> FEATURE:
164 <223> OTHER INFORMATION: Synthesized sequence, primer Sig
165 mb
W--> 166 <400> SEQUENCE: 15
E--> 167 cgtacgaatg acgtgccct gcgaatcgta cg *same*
168 32
169 <210> SEQ ID NO: 16
170 <211> LENGTH: 49
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial sequence
W--> 173 <220> FEATURE:
174 <223> OTHER INFORMATION: Synthesized sequence, primer TIE
175 p1
W--> 176 <400> SEQUENCE: 16
E--> 177 aattctaata cgactcacta tagggaagag *same*
178 ctctctcctg ttggtccct 49
179 <210> SEQ ID NO: 17
180 <211> LENGTH: 24
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial sequence
W--> 183 <220> FEATURE:
184 <223> OTHER INFORMATION: Synthesized sequence, primer TIE
185 p2
W--> 186 <400> SEQUENCE: 17
E--> 187 gcattctctgt tcatgactgt gtga *same*
188 24
189 <210> SEQ ID NO: 18
190 <211> LENGTH: 33
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial sequence
W--> 193 <220> FEATURE:

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11192003\J700380.raw

194 <223> OTHER INFORMATION: Synthesized sequence, primer TIE

195 mb

W--> 196 <400> SEQUENCE: 18

E--> 197 cgtacgctca acgccagcac gcgctaccgt acg

198 33



VERIFICATION SUMMARY

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11192003\J700380.raw

L:8 M:283 W: Missing Blank Line separator, <120> field identifier
L:10 M:283 W: Missing Blank Line separator, <130> field identifier
L:11 M:283 W: Missing Blank Line separator, <140> field identifier
L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:17 M:283 W: Missing Blank Line separator, <160> field identifier
L:19 M:283 W: Missing Blank Line separator, <210> field identifier
L:23 M:283 W: Missing Blank Line separator, <220> field identifier
L:26 M:283 W: Missing Blank Line separator, <400> field identifier
L:27 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:1
L:33 M:283 W: Missing Blank Line separator, <220> field identifier
L:36 M:283 W: Missing Blank Line separator, <400> field identifier
L:37 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:2
L:43 M:283 W: Missing Blank Line separator, <220> field identifier
L:45 M:283 W: Missing Blank Line separator, <400> field identifier
L:46 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:3
L:52 M:283 W: Missing Blank Line separator, <220> field identifier
L:57 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:4
L:63 M:283 W: Missing Blank Line separator, <220> field identifier
L:66 M:283 W: Missing Blank Line separator, <400> field identifier
L:67 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:5
L:73 M:283 W: Missing Blank Line separator, <220> field identifier
L:76 M:283 W: Missing Blank Line separator, <400> field identifier
L:77 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:6
L:83 M:283 W: Missing Blank Line separator, <220> field identifier
L:86 M:283 W: Missing Blank Line separator, <400> field identifier
L:87 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:7
L:93 M:283 W: Missing Blank Line separator, <220> field identifier
L:96 M:283 W: Missing Blank Line separator, <400> field identifier
L:97 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:8
L:103 M:283 W: Missing Blank Line separator, <220> field identifier
L:106 M:283 W: Missing Blank Line separator, <400> field identifier
L:107 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:34 SEQ:9
L:113 M:283 W: Missing Blank Line separator, <220> field identifier
L:116 M:283 W: Missing Blank Line separator, <400> field identifier
L:117 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:34 SEQ:10
L:123 M:283 W: Missing Blank Line separator, <220> field identifier
L:126 M:283 W: Missing Blank Line separator, <400> field identifier
L:127 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:11
L:133 M:283 W: Missing Blank Line separator, <220> field identifier
L:136 M:283 W: Missing Blank Line separator, <400> field identifier
L:137 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:12
L:143 M:283 W: Missing Blank Line separator, <220> field identifier
L:146 M:283 W: Missing Blank Line separator, <400> field identifier
L:147 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:13
L:153 M:283 W: Missing Blank Line separator, <220> field identifier
L:156 M:283 W: Missing Blank Line separator, <400> field identifier
L:157 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:14
L:163 M:283 W: Missing Blank Line separator, <220> field identifier

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11192003\J700380.raw

L:166 M:283 W: Missing Blank Line separator, <400> field identifier
L:167 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:15
L:173 M:283 W: Missing Blank Line separator, <220> field identifier
L:176 M:283 W: Missing Blank Line separator, <400> field identifier
L:177 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:16
L:183 M:283 W: Missing Blank Line separator, <220> field identifier
L:186 M:283 W: Missing Blank Line separator, <400> field identifier
L:187 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:17
L:193 M:283 W: Missing Blank Line separator, <220> field identifier
L:196 M:283 W: Missing Blank Line separator, <400> field identifier
L:197 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:18